

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/664,025A
Source: FW/6
Date Processed by STIC: 9/22/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/22/2006

PATENT APPLICATION: US/10/664,025A

TIME: 11:05:03

Input Set : F:\G-077US03DIV-Seq-List-replace.TXT

Output Set: N:\CRF4\09222006\J664025A.raw

3 <110> APPLICANT: Dumas Milne Edwards, J.B.
 4 Jobert, S.
 5 Giordano, J.Y.

W--> 6 <120> TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 W--> 7 <130> FILE REFERENCE: GENSET.054PR2
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/664,025A
 C--> 8 <141> CURRENT FILING DATE: 2003-09-15
 W--> 8 <160> NUMBER OF SEQ ID: 19379
 9 <170> SOFTWARE: Patent.pm

W--> 10 <210> SEQ ID NO: 1
 11 <211> LENGTH: 822
 12 <212> TYPE: DNA
 13 <213> ORGANISM: Homo Sapiens

W--> 14 <220> FEATURE:
 15 <221> NAME/KEY: CDS
 16 <222> LOCATION: 346..552

W--> 17 <220> FEATURE:
 18 <221> NAME/KEY: sig_peptide
 19 <222> LOCATION: 346..408
 20 <223> OTHER INFORMATION: Von Heijne matrix

W--> 21 <220> FEATURE:
 22 <221> NAME/KEY: misc_feature
 23 <222> LOCATION: 115
 24 <223> OTHER INFORMATION: n=a, g, c or t

W--> 25 <400> SEQUENCE: 1

26	actccttttta gcataggggc ttcggcgcgcca gcgccagcg ctagtcgggtc tggtaagtgc	60
W--> 27	ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc	120
28	ctcaaacggc ctagtgcttc gcgcttcgag agaaaatcag cggcttaatt aattcctctg	180
29	gtttgttgaa gcagttacca agaattcttca accctttccc acaaaaagcta attgagtaca	240
30	cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg	300
31	aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt	357
32		
33	Met Trp Trp Phe	
	-20	
34	cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct	405
35	Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser	
36	-15 -10 -5	
37	gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata	453
38	Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile	
39	1 5 10 15	
40	gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa	501
41	Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa	
42	20 25 30	
43	aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa	549

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44 Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
45          35          40          45
46 aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa      602
47 Lys
48 ctcttcaraa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      662
49 gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg      722
50 gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw      782
51 tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa      822
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 21
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo Sapiens
W--> 56 <220> FEATURE:
57 <221> NAME/KEY: SIGNAL
58 <222> LOCATION: -21..-1
W--> 59 <400> SEQUENCE: 2
60 Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
61      -20          -15          -10
62 Ile Trp Thr Ser Ala
63 -5
64 <210> SEQ ID NO: 3
65 <211> LENGTH: 526
66 <212> TYPE: DNA
67 <213> ORGANISM: Homo Sapiens
W--> 68 <220> FEATURE:
69 <221> NAME/KEY: CDS
70 <222> LOCATION: 90..344
W--> 71 <220> FEATURE:
72 <221> NAME/KEY: sig_peptide
73 <222> LOCATION: 90..140
74 <223> OTHER INFORMATION: Von Heijne matrix
W--> 75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: 290
78 <223> OTHER INFORMATION: n=a, g, c or t
W--> 79 <400> SEQUENCE: 3
80 aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca      60
81 gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc      113
82          Met Lys Lys Val Leu Leu Leu Ile
83          -15          -10
84 aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
85 Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
86          -5          1          5
87 gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr      209
88 Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
89      10          15          20
90 wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att      257
W--> 91 Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
92      25          30          35

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93 cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata      305
94 Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
95 40                      45                      50                      55
96 cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa      354
97 Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
98                      60                      65
99 ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat      414
100 caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta      474
101 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa      526
102 <210> SEQ ID NO: 4
103 <211> LENGTH: 17
104 <212> TYPE: PRT
105 <213> ORGANISM: Homo Sapiens
W--> 106 <220> FEATURE:
107 <221> NAME/KEY: SIGNAL
108 <222> LOCATION: -17..-1
W--> 109 <400> SEQUENCE: 4
110 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
111      -15                      -10                      -5
112 Gly
113 <210> SEQ ID NO: 5
114 <211> LENGTH: 848
115 <212> TYPE: DNA
116 <213> ORGANISM: Homo Sapiens
W--> 117 <220> FEATURE:
118 <221> NAME/KEY: CDS
119 <222> LOCATION: 32..697
W--> 120 <220> FEATURE:
121 <221> NAME/KEY: sig_peptide
122 <222> LOCATION: 32..73
123 <223> OTHER INFORMATION: Von Heijne matrix
W--> 124 <400> SEQUENCE: 5
125 aactttgcct tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt      52
126                      Met Leu Trp Leu Leu Phe Phe
127                      -10
128 ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat      100
129 Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
130      -5                      1                      5
131 gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca      148
132 Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
133 10                      15                      20                      25
134 tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct      196
135 Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
136      30                      35                      40
137 ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat      244
138 Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
139      45                      50                      55
140 gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt      292
141 Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val

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```

142          60          65          70
143 aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca      340
144 Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
145          75          80          85
146 gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat      388
147 Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
148 90          95          100          105
149 gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc      436
150 Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
151          110          115          120
152 atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt      484
153 Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
154          125          130          135
155 tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg      532
156 Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
157          140          145          150
158 caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa      580
W--> 159 Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
160          155          160          165
161 rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat      628
162 Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
163 170          175          180          185
164 ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag      676
165 Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
166          190          195          200
167 gat gag agg ctc acc cct ctc tgaagggtg ttgttctgct tcctcaaraa      727
168 Asp Glu Arg Leu Thr Pro Leu
169          205
170 attaaacatt tgtttctgtg tgactgctga gcacacctgaa ataccaagag cagatcatat      787
171 wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa      847
172 c      848
173 <210> SEQ ID NO: 6
174 <211> LENGTH: 14
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo Sapiens
W--> 177 <220> FEATURE:
178 <221> NAME/KEY: SIGNAL
179 <222> LOCATION: -14..-1
W--> 180 <400> SEQUENCE: 6
181 Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
182          -10          -5
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 826
185 <212> TYPE: DNA
186 <213> ORGANISM: Homo sapiens
W--> 187 <220> FEATURE:
188 <221> NAME/KEY: CDS
189 <222> LOCATION: 15..695
W--> 190 <220> FEATURE:

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191 <221> NAME/KEY: sig_peptide
192 <222> LOCATION: 15..80
193 <223> OTHER INFORMATION: Von Heijne matrix
194     score 8.5
195     seq AALLLGLMMVVTG/DE
W--> 196 <400> SEQUENCE: 7
197 aaccagaggt gccg atg ggt tgg aca atg agg ctg gtc aca gca gca ctg      50
198           Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
199           -20                               -15
200 tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc      98
201 Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
202 -10                               -5                               1                               5
203 ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag      146
204 Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
205           10                               15                               20
206 ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt      194
207 Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
208           25                               30                               35
209 gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag      242
210 Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
211           40                               45                               50
212 ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg      290
213 Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
214 55                               60                               65                               70
215 gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
216 Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
217           75                               80                               85
218 ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
219 Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
220           90                               95                               100
221 aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
222 Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
223           105                               110                               115
224 cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
225 Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
226           120                               125                               130
227 cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
228 Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
229 135                               140                               145                               150
230 ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
231 Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
232           155                               160                               165
233 cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
234 Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
235           170                               175                               180
236 acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
237 Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
238           185                               190                               195
239 cag gcg gag ata gct gcc tgc tagatagccg gctttgccat cgggcatgt      725

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 115
Seq#:1; Xaa Pos. 31
Seq#:3; N Pos. 290
Seq#:3; Xaa Pos. 24,50
Seq#:5; Xaa Pos. 156,157,170,171
Seq#:20; N Pos. 335,376
Seq#:24; Xaa Pos. 6
Seq#:25; N Pos. 25
Seq#:25; Xaa Pos. 16,17
Seq#:27; Xaa Pos. -10
Seq#:30; Xaa Pos. -24,7,13
Seq#:31; Xaa Pos. 13
Seq#:33; Xaa Pos. 9
Seq#:34; Xaa Pos. -5,9,11,12,18,19,26
Seq#:35; N Pos. 9
Seq#:35; Xaa Pos. -5
Seq#:36; Xaa Pos. 2
Seq#:38; Xaa Pos. 18,19,45,47,55
Seq#:39; Xaa Pos. 30
Seq#:41; Xaa Pos. -15,7
Seq#:42; Xaa Pos. 28,52,54,96,101,105
Seq#:46; N Pos. 8
Seq#:46; Xaa Pos. 119
Seq#:48; Xaa Pos. -18
Seq#:50; N Pos. 236,237
Seq#:50; Xaa Pos. -32,-30,-28,-25,-20,-17,-16,5,9,16
Seq#:52; Xaa Pos. 78
Seq#:54; Xaa Pos. 83
Seq#:55; Xaa Pos. 54,56,59
Seq#:58; Xaa Pos. -14,9,24,36
Seq#:60; Xaa Pos. -20
Seq#:61; Xaa Pos. 28,48
Seq#:62; Xaa Pos. -25
Seq#:63; Xaa Pos. -15,7,8,27
Seq#:67; Xaa Pos. 35
Seq#:69; Xaa Pos. 50,101
Seq#:71; Xaa Pos. 35
Seq#:73; Xaa Pos. 28,41,42
Seq#:74; Xaa Pos. 26
Seq#:75; Xaa Pos. 26
Seq#:77; N Pos. 12
Seq#:77; Xaa Pos. 24
Seq#:79; N Pos. 10,360
Seq#:79; Xaa Pos. 24

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Input Set : F:\G-077US03DIV-Seq-List-replace.TXT
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Seq#:80; N Pos. 233
Seq#:80; Xaa Pos. 1
Seq#:81; Xaa Pos. 41
Seq#:82; Xaa Pos. 46
Seq#:84; Xaa Pos. 22
Seq#:88; N Pos. 89,90,95,255
Seq#:88; Xaa Pos. -72,-39,-28,-22,-8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4846; Line(s) 147297
Seq#:6835; Line(s) 186255

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Input Set : F:\G-077US03DIV-Seq-List-replace.TXT

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L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:27 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:60
M:341 Repeated in SeqNo=1
L:56 M:283 W: Missing Blank Line separator, <220> field identifier
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <220> field identifier
L:75 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:257
M:341 Repeated in SeqNo=3
L:106 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:283 W: Missing Blank Line separator, <220> field identifier
L:124 M:283 W: Missing Blank Line separator, <400> field identifier
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:580
M:341 Repeated in SeqNo=5
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:180 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:283 W: Missing Blank Line separator, <220> field identifier
L:190 M:283 W: Missing Blank Line separator, <220> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:248 M:283 W: Missing Blank Line separator, <220> field identifier
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:286 M:283 W: Missing Blank Line separator, <220> field identifier
L:289 M:283 W: Missing Blank Line separator, <220> field identifier
L:295 M:283 W: Missing Blank Line separator, <400> field identifier
L:358 M:283 W: Missing Blank Line separator, <220> field identifier
L:361 M:283 W: Missing Blank Line separator, <400> field identifier
L:403 M:283 W: Missing Blank Line separator, <220> field identifier
L:406 M:283 W: Missing Blank Line separator, <220> field identifier
L:412 M:283 W: Missing Blank Line separator, <400> field identifier
L:438 M:283 W: Missing Blank Line separator, <220> field identifier
L:441 M:283 W: Missing Blank Line separator, <400> field identifier
L:456 M:283 W: Missing Blank Line separator, <220> field identifier
L:459 M:283 W: Missing Blank Line separator, <220> field identifier
L:465 M:283 W: Missing Blank Line separator, <400> field identifier
L:510 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : F:\G-077US03DIV-Seq-List-replace.TXT

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L:513 M:283 W: Missing Blank Line separator, <400> field identifier
L:534 M:283 W: Missing Blank Line separator, <220> field identifier
L:536 M:283 W: Missing Blank Line separator, <400> field identifier
L:542 M:283 W: Missing Blank Line separator, <220> field identifier
L:544 M:283 W: Missing Blank Line separator, <400> field identifier
L:550 M:283 W: Missing Blank Line separator, <220> field identifier
L:553 M:283 W: Missing Blank Line separator, <220> field identifier
L:557 M:283 W: Missing Blank Line separator, <220> field identifier
L:564 M:283 W: Missing Blank Line separator, <220> field identifier
L:571 M:283 W: Missing Blank Line separator, <220> field identifier
L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:300
M:341 Repeated in SeqNo=20
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:213
L:1054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:1145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:407
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:177
M:341 Repeated in SeqNo=30
L:1287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:201
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:270
L:1415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:286
M:341 Repeated in SeqNo=34
L:1444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
M:341 Repeated in SeqNo=35
L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:343
L:1571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:208
M:341 Repeated in SeqNo=38
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:259
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:113
M:341 Repeated in SeqNo=41
L:1739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:196
M:341 Repeated in SeqNo=42
L:1892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
M:341 Repeated in SeqNo=46
L:1985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:351
L:2067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:200
M:341 Repeated in SeqNo=50
L:2156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:402
L:2242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:341
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:484
M:341 Repeated in SeqNo=55
L:2394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:222
M:341 Repeated in SeqNo=58
L:2457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:159
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:198
M:341 Repeated in SeqNo=61
L:2515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:57
L:2551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:222
M:341 Repeated in SeqNo=63

VERIFICATION SUMMARY

DATE: 09/22/2006

PATENT APPLICATION: US/10/664,025A

TIME: 11:05:04

Input Set : F:\G-077US03DIV-Seq-List-replace.TXT

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L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:478
L:2754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:302
M:341 Repeated in SeqNo=69
L:2825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:329
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:199
L:15224 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:390
L:15244 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:391
L:15279 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:392
L:15305 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:393
L:15679 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:405
L:15792 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:408
L:15846 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:410
L:15872 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:411
L:15957 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:414
L:16032 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:416
L:16088 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:418
L:16105 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:419
L:16262 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:424
L:16290 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:425
L:16385 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:429
L:16520 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:433
L:16658 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:438
L:16691 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:439
L:16725 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:440
L:16756 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:441
L:16846 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:444
L:17450 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:462
L:17504 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:464
L:17757 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:472
L:17804 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:473
L:17852 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:475
L:17912 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:477
L:18051 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:482
L:18110 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:484
L:18165 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:486
L:18196 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:487
L:18333 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:492
L:18369 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:493
L:18622 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:502
L:18684 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:504
L:18790 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:507
L:18937 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:512
L:18955 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:513
L:19364 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:526
L:19418 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:527
L:19481 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:529
L:19607 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:534
L:19699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:537
L:19888 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:543

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L:19915 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:544
L:20069 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:549
L:20356 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:558
L:21062 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:581
L:21131 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:583
L:21167 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:584